

SEQUENCE LISTING

<110> Rosen et al.

<120> Antibodies Against Protective Antigen

<130> PF596P1N

<150> 60/391,162

<151> 2002-06-26

<150> 60/406,339

<151> 2002-08-28

<150> 60/417,305

<151> 2002-10-10

<150> 60/426,360

<151> 2002-11-15

<150> 60/434,807

<151> 2002-12-20

<150> 60/438,004

<151> 2003-01-06

<150> 60/443,858

<151> 2003-01-31

<150> 60/443,781

<151> 2003-01-31

<150> 60/454,613

<151> 2003-03-17

<150> 60/468,651

<151> 2003-05-08

<160> 65

<170> PatentIn version 3.1

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<212> DNA

<213> Bacillus anthracis

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48

ctg gtt tct agc acc ggt aac ctg gaa gta atc cag gct gaa gtt aaa Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys	96
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cag gaa aac cgt ctg ctc aac gaa tct gag tct tcc tct cag ggc ctg Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu	144
35 40 45	
ctg ggt tac tat ttc tct gac ctg aac ttc cag gca ccg atg gtt gta Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val	192
50 55 60	
act tct tcc acc acc ggc gac ctg tct att ccg tct tct gaa ctg gag Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu	240
65 70 75 80	
aac atc ccg tct gaa aac cag tac ttc cag tct gct atc tgg tct ggt Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly	288
85 90 95	
ttc att aaa gtt aag aaa tct gac gaa tac acc ttc gct act tct gca Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala	336
100 105 110	
gat aac cac gtt act atg tgg gta gac gac cag gaa gtt atc aac aaa Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys	384
115 120 125	
gct tct aac tct aac aaa atc cgt ctg gaa aaa ggc cgt ctg tac cag Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln	432
130 135 140	
atc aag att caa tac caa cgt gaa aac ccg acc gag aaa ggt ctg gac Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp	480
145 150 155 160	
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165 170 175	
tcc gac aac ctg cag ctg ccg gaa ctg aaa cag aaa tct tcc aac tct Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser	576
180 185 190	
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195 200 205	
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210 215 220	
gtt aaa aac aaa cgt acc ttc ctg tct ccg tgg atc tct aac atc cac Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His	720
225 230 235 240	
gaa aag aaa ggt ctg acc aaa tac aaa tct tcc ccg gag aaa tgg tct Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser	768
245 250 255	

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gac aaa aac gtt tct ccg gaa gct cgt cac ccg ctg gta gca gcg tac Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr 275 280 285	864
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gac cag tct acc cag aac acc gac tct caa act cgt acc atc tct aaa Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys 305 310 315 320	960
aac acc tct acc tct cgt act cac acc tct gaa gtt cac ggt aac gct Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala 325 330 335	1008
gag gtt cac gct tct ttc ttt gac atc ggt ggc tct gta tct gct ggt Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly 340 345 350	1056
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ctg gct ggt gaa cgt acc tgg gct gaa act atg ggc ctg aac acc gca Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala 370 375 380	1152
gac acc gct cgt ctg aac gct aac atc cgt tac gtt aac acc ggc acc Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr 385 390 395 400	1200
gct ccg atc tac aac gtt ctg ccg act acc tct ctg gta ctg ggt aaa Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys 405 410 415	1248
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gca ctg aac gct cag gac gac ttc tct tcc acc ccg atc act atg aac Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn 450 455 460	1392
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acc gac cag gtt tac ggt aac atc gct acc tac aac ttc gaa aac ggt Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly 485 490 495	1488

cgt gtt cgt gta gac acc ggc tct aac tgg tct gaa gtt ctg ccg cag	1536
Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln	
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atc cag gaa acc act gct cgt att atc ttc aac ggt aaa gac ctg aac	1584
Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn	
515 520 525	
ctg gtt gaa cgt cgt atc gct gca gta aac ccg tct gac ccg ctg gaa	1632
Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu	
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acc act aaa ccg gac atg acc ctg aaa gaa gct ctg aaa atc gct ttc	1680
Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe	
545 550 555 560	
ggg ttc aac gaa ccg aac ggc aac ctg cag tac cag ggt aaa gat atc	1728
Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile	
565 570 575	
acc gaa ttc gac ttt aac ttc gac cag caa acc tct cag aac atc aaa	1776
Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys	
580 585 590	
aac cag ctg gct gaa ctg aac gct acc aac atc tac acc gtt ctg gac	1824
Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp	
595 600 605	
aaa atc aag ctg aac gct aaa atg aac att ctg atc cgt gat aaa cgt	1872
Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg	
610 615 620	
ttc cac tac gac cgt aac aac atc gct gtt ggt gct gac gaa tct gta	1920
Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val	
625 630 635 640	
gtt aaa gaa gct cac cgt gag gtt atc aac tct tcc acc gaa ggt ctg	1968
Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu	
645 650 655	
ctc ctg aac atc gac aaa gat att cgt aaa atc ctg tct ggt tac atc	2016
Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile	
660 665 670	
gtt gaa atc gaa gac acc gag ggc ctg aaa gaa gtt atc aac gac cgt	2064
Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg	
675 680 685	
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Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe	
690 695 700	
atc gac ttc aaa aag tac aac gat aaa ctg ccg ctg tac atc tct aac	2160
Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn	
705 710 715 720	
ccg aac tac aaa gta aac gtt tac gct gtt acc aaa gaa aac acc att	2208
Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile	
725 730 735	

atc aac ccg tct gaa aac ggt gac acc tct acc aac ggt atc aaa aag 2256
 Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
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atc ctg atc ttc tct aag aaa ggc tac gaa atc ggt taa 2295
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 35 40 45
 Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val
 50 55 60
 Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu
 65 70 75 80
 Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly
 85 90 95
 Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala
 100 105 110
 Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys
 115 120 125
 Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln
 130 135 140
 Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp
 145 150 155 160
 Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser
 165 170 175
 Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser
 180 185 190
 Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp
 195 200 205
 Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp
 210 215 220
 Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His
 225 230 235 240

Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser
 245 250 255
 Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile
 260 265 270
 Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr
 275 280 285
 Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu
 290 295 300
 Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys
 305 310 315 320
 Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala
 325 330 335
 Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly
 340 345 350
 Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser
 355 360 365
 Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala
 370 375 380
 Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr
 385 390 395 400
 Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys
 405 410 415
 Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln
 420 425 430
 Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile
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 Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn
 450 455 460
 Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp
 465 470 475 480
 Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly
 485 490 495
 Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln
 500 505 510
 Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn
 515 520 525
 Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu
 530 535 540
 Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe
 545 550 555 560

Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile
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 Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys
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 Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp
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 Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val
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 Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu
 645 650 655
 Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile
 660 665 670
 Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
 675 680 685
 Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
 690 695 700
 Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
 705 710 715 720
 Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
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 35 40 45
 Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
 50 55 60
 Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met

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Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr	85					90					95				
Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val	100					105					110				
Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser	115					120					125				
Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val	130					135					140				
Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr	145					150					155				
Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr	165					170					175				
Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala	180					185					190				
Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu	195					200					205				
Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu	210					215					220				
Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val	225					230					235				
Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu	245					250					255				
Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe	260					265					270				
Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu	275					280					285				
Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser	290					295					300				
Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly	305					310					315				
Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu	325					330					335				
Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys	340					345					350				
Glu Val Pro Pro Pro Pro Ala Glu Glu Ser Glu Glu Asn Lys Ile Lys	355					360					365				

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Ala Met Asn Glu His Tyr Thr Glu Ser Asp Ile Lys Arg Asn His Lys
35 40 45

Thr Glu Lys Asn Lys Thr Glu Lys Glu Lys Phe Lys Asp Ser Ile Asn
50 55 60

Asn Leu Val Lys Thr Glu Phe Thr Asn Glu Thr Leu Asp Lys Ile Gln
65 70 75 80

Gln Thr Gln Asp Leu Leu Lys Lys Ile Pro Lys Asp Val Leu Glu Ile
85 90 95

Tyr Ser Glu Leu Gly Gly Glu Ile Tyr Phe Thr Asp Ile Asp Leu Val
100 105 110

Glu His Lys Glu Leu Gln Asp Leu Ser Glu Glu Glu Lys Asn Ser Met
115 120 125

Asn Ser Arg Gly Glu Lys Val Pro Phe Ala Ser Arg Phe Val Phe Glu
130 135 140

Lys Lys Arg Glu Thr Pro Lys Leu Ile Ile Asn Ile Lys Asp Tyr Ala
145 150 155 160

Ile Asn Ser Glu Gln Ser Lys Glu Val Tyr Tyr Glu Ile Gly Lys Gly
165 170 175

Ile Ser Leu Asp Ile Ile Ser Lys Asp Lys Ser Leu Asp Pro Glu Phe
180 185 190

Leu Asn Leu Ile Lys Ser Leu Ser Asp Asp Ser Asp Ser Ser Asp Leu
195 200 205

Leu Phe Ser Gln Lys Phe Lys Glu Lys Leu Glu Leu Asn Asn Lys Ser
210 215 220

Ile Asp Ile Asn Phe Ile Lys Glu Asn Leu Thr Glu Phe Gln His Ala
225 230 235 240

Phe Ser Leu Ala Phe Ser Tyr Tyr Phe Ala Pro Asp His Arg Thr Val
245 250 255

Leu Glu Leu Tyr Ala Pro Asp Met Phe Glu Tyr Met Asn Lys Leu Glu
260 265 270

Lys Gly Gly Phe Glu Lys Ile Ser Glu Ser Leu Lys Lys Glu Gly Val
275 280 285

Glu Lys Asp Arg Ile Asp Val Leu Lys Gly Glu Lys Ala Leu Lys Ala
290 295 300

Ser Gly Leu Val Pro Glu His Ala Asp Ala Phe Lys Lys Ile Ala Arg
 305 310 315 320
 Glu Leu Asn Thr Tyr Ile Leu Phe Arg Pro Val Asn Lys Leu Ala Thr
 325 330 335
 Asn Leu Ile Lys Ser Gly Val Ala Thr Lys Gly Leu Asn Val His Gly
 340 345 350
 Lys Ser Ser Asp Trp Gly Pro Val Ala Gly Tyr Ile Pro Phe Asp Gln
 355 360 365
 Asp Leu Ser Lys Lys His Gly Gln Gln Leu Ala Val Glu Lys Gly Asn
 370 375 380
 Leu Glu Asn Lys Lys Ser Ile Thr Glu His Glu Gly Glu Ile Gly Lys
 385 390 395 400
 Ile Pro Leu Lys Leu Asp His Leu Arg Ile Glu Glu Leu Lys Glu Asn
 405 410 415
 Gly Ile Ile Leu Lys Gly Lys Lys Glu Ile Asp Asn Gly Lys Lys Tyr
 420 425 430
 Tyr Leu Leu Glu Ser Asn Asn Gln Val Tyr Glu Phe Arg Ile Ser Asp
 435 440 445
 Glu Asn Asn Glu Val Gln Tyr Lys Thr Lys Glu Gly Lys Ile Thr Val
 450 455 460
 Leu Gly Glu Lys Phe Asn Trp Arg Asn Ile Glu Val Met Ala Lys Asn
 465 470 475 480
 Val Glu Gly Val Leu Lys Pro Leu Thr Ala Asp Tyr Asp Leu Phe Ala
 485 490 495
 Leu Ala Pro Ser Leu Thr Glu Ile Lys Lys Gln Ile Pro Gln Lys Glu
 500 505 510
 Trp Asp Lys Val Val Asn Thr Pro Asn Ser Leu Glu Lys Gln Lys Gly
 515 520 525
 Val Thr Asn Leu Leu Ile Lys Tyr Gly Ile Glu Arg Lys Pro Asp Ser
 530 535 540
 Thr Lys Gly Thr Leu Ser Asn Trp Gln Lys Gln Met Leu Asp Arg Leu
 545 550 555 560
 Asn Glu Ala Val Lys Tyr Thr Gly Tyr Thr Gly Gly Asp Val Val Asn
 565 570 575
 His Gly Thr Glu Gln Asp Asn Glu Glu Phe Pro Glu Lys Asp Asn Glu
 580 585 590
 Ile Phe Ile Ile Asn Pro Glu Gly Glu Phe Ile Leu Thr Lys Asn Trp
 595 600 605
 Glu Met Thr Gly Arg Phe Ile Glu Lys Asn Ile Thr Gly Lys Asp Tyr
 610 615 620

Leu Tyr Tyr Phe Asn Arg Ser Tyr Asn Lys Ile Ala Pro Gly Asn Lys
625 630 635 640

Ala Tyr Ile Glu Trp Thr Asp Pro Ile Thr Lys Ala Lys Ile Asn Thr
645 650 655

Ile Pro Thr Ser Ala Glu Phe Ile Lys Asn Leu Ser Ser Ile Arg Arg
660 665 670

Ser Ser Asn Val Gly Val Tyr Lys Asp Ser Gly Asp Lys Asp Glu Phe
675 680 685

Ala Lys Lys Glu Ser Val Lys Lys Ile Ala Gly Tyr Leu Ser Asp Tyr
690 695 700

Tyr Asn Ser Ala Asn His Ile Phe Ser Gln Glu Lys Lys Arg Lys Ile
705 710 715 720

Ser Ile Phe Arg Gly Ile Gln Ala Tyr Asn Glu Ile Glu Asn Val Leu
725 730 735

Lys Ser Lys Gln Ile Ala Pro Glu Tyr Lys Asn Tyr Phe Gln Tyr Leu
740 745 750

Lys Glu Arg Ile Thr Asn Gln Val Gln Leu Leu Leu Thr His Gln Lys
755 760 765

Ser Asn Ile Glu Phe Lys Leu Leu Tyr Lys Gln Leu Asn Phe Thr Glu
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785 790 795 800

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Gly Ala Gly Gly His Gly Asp Val Gly Met His Val Lys Glu Lys Glu
35 40 45

Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu Glu Arg Asn Lys Thr
50 55 60

Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile Val Lys Ile Glu
65 70 75 80

Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala Glu Lys Leu Leu
85 90 95

Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys Ala Ile Gly Gly
100 105 110

Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr Lys His Ile Ser Leu Glu
 115 120 125
 Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys Asp Ile Tyr Gly Lys Asp
 130 135 140
 Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys Glu Gly Tyr Glu Pro
 145 150 155 160
 Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val Glu Asn Thr Glu Lys
 165 170 175
 Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu Ser Arg Asp Ile
 180 185 190
 Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu Asp Val Leu Asn
 195 200 205
 Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp Leu Leu Phe Thr
 210 215 220
 Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val Glu Phe Leu Glu
 225 230 235 240
 Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys Ala Phe Ala Tyr
 245 250 255
 Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu Tyr Ala Pro Glu
 260 265 270
 Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu Ile Asn Leu Ser
 275 280 285
 Leu Glu Glu Leu Lys Asp Gln Arg Met Leu Ser Arg Tyr Glu Lys Trp
 290 295 300
 Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu
 305 310 315 320
 Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys
 325 330 335
 Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu
 340 345 350
 Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys
 355 360 365
 Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu
 370 375 380
 Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro
 385 390 395 400
 Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile
 405 410 415
 Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile
 420 425 430

Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp
 435 440 445
 Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu
 450 455 460
 Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr
 465 470 475 480
 Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile
 485 490 495
 Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile
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 Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp
 515 520 525
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 Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu
 545 550 555 560
 Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile
 565 570 575
 Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile
 580 585 590
 Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly
 595 600 605
 Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr
 610 615 620
 Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys
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 Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val
 645 650 655
 Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile
 660 665 670
 Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser
 675 680 685
 Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro
 690 695 700
 Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu
 705 710 715 720
 Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn
 725 730 735
 Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys
 740 745 750

Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu
755 760 765

Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu
770 775 780

Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn
785 790 795 800

Asp Gln Ile Lys Phe Ile Ile Asn Ser
805

<210> 6
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer useful for amplifying VH and VL domains

<400> 6
caggtgcagc tgggtgcagtc tgg 23

<210> 7
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer useful for amplifying VH and VL domains

<400> 7
caggtcaact taagggagtc tgg 23

<210> 8
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer useful for amplifying VH and VL domains

<400> 8
gaggtgcagc tgggtggagtc tgg 23

<210> 9
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer useful for amplifying VH and VL domains

<400> 9
caggtgcagc tgcaggagtc ggg 23

<210> 10
<211> 23
<212> DNA
<213> Artificial sequence

<220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 10
 gaggtgcagc tgttcgagtc tgc 23

 <210> 11
 <211> 23
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 11
 caggtacagc tgcagcagtc agg 23

 <210> 12
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 12
 tgaggagacg gtgaccaggg tgcc 24

 <210> 13
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 13
 tgaagagacg gtgaccattg tccc 24

 <210> 14
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 14
 tgaggagacg gtgaccaggg ttcc 24

 <210> 15
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 15

tgaggagacg gtgaccgtgg tccc 24

<210> 16
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer useful for amplifying VH and VL domains

<400> 16
 gacatccaga tgacccagtc tcc 23

<210> 17
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer useful for amplifying VH and VL domains

<400> 17
 gatgttgtga tgactcagtc tcc 23

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer useful for amplifying VH and VL domains

<400> 18
 gatattgtga tgactcagtc tcc 23

<210> 19
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer useful for amplifying VH and VL domains

<400> 19
 gaaattgtgt tgacgcagtc tcc 23

<210> 20
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer useful for amplifying VH and VL domains

<400> 20
 gacatcgtga tgacccagtc tcc 23

<210> 21
 <211> 23
 <212> DNA

<213> Artificial sequence

<220>

<223> PCR primer useful for amplifying VH and VL domains

<400> 21

gaaacgacac tcacgcagtc tcc

23

<210> 22

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer useful for amplifying VH and VL domains

<400> 22

gaaattgtgc tgactcagtc tcc

23

<210> 23

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer useful for amplifying VH and VL domains

<400> 23

cagtctgtgt tgacgcagcc gcc

23

<210> 24

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer useful for amplifying VH and VL domains

<400> 24

cagtctgccc tgactcagcc tgc

23

<210> 25

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer useful for amplifying VH and VL domains

<400> 25

tcctatgtgc tgactcagcc acc

23

<210> 26

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer useful for amplifying VH and VL domains

<400> 26
 tcttctgagc tgactcagga ccc 23

 <210> 27
 <211> 23
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 27
 cacgttatac tgactcaacc gcc 23

 <210> 28
 <211> 23
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 28
 caggtgtgc tcactcagcc gtc 23

 <210> 29
 <211> 23
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 29
 aattttatgc tgactcagcc cca 23

 <210> 30
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 30
 acgtttgatt tccaccttgg tccc 24

 <210> 31
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 31
 acgtttgatc tccagcttgg tccc 24

 <210> 32
 <211> 24

<212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 32
 acgtttgata tccactttgg tccc 24

 <210> 33
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 33
 acgtttgatc tccaccttgg tccc 24

 <210> 34
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 34
 acgtttaatc tccagtcgtg tccc 24

 <210> 35
 <211> 23
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 35
 cagtctgtgt tgacgcagcc gcc 23

 <210> 36
 <211> 23
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

 <400> 36
 cagtctgccc tgactcagcc tgc 23

 <210> 37
 <211> 23
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> PCR primer useful for amplifying VH and VL domains

<400> 37
tcctatgtgc tgactcagcc acc 23

<210> 38
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer useful for amplifying VH and VL domains

<400> 38
tcttctgagc tgactcagga ccc 23

<210> 39
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer useful for amplifying VH and VL domains

<400> 39
cacgttatac tgactcaacc gcc 23

<210> 40
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer useful for amplifying VH and VL domains

<400> 40
caggctgtgc tcactcagcc gtc 23

<210> 41
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer useful for amplifying VH and VL domains

<400> 41
aattttatgc tgactcagcc cca 23

<210> 42
<211> 489
<212> PRT
<213> Homo sapiens

<400> 42
Met Val Ala Glu Arg Ser Pro Ala Arg Ser Pro Gly Ser Trp Leu Phe
1 5 10 15
Pro Gly Leu Trp Leu Leu Val Leu Ser Gly Pro Gly Gly Leu Leu Arg
20 25 30

Ala Gln Glu Gln Pro Ser Cys Arg Arg Ala Phe Asp Leu Tyr Phe Val
 35 40 45
 Leu Asp Lys Ser Gly Ser Val Ala Asn Asn Trp Ile Glu Ile Tyr Asn
 50 55 60
 Phe Val Gln Gln Leu Ala Glu Arg Phe Val Ser Pro Glu Met Arg Leu
 65 70 75 80
 Ser Phe Ile Val Phe Ser Ser Gln Ala Thr Ile Ile Leu Pro Leu Thr
 85 90 95
 Gly Asp Arg Gly Lys Ile Ser Lys Gly Leu Glu Asp Leu Lys Arg Val
 100 105 110
 Ser Pro Val Gly Glu Thr Tyr Ile His Glu Gly Leu Lys Leu Ala Asn
 115 120 125
 Glu Gln Ile Gln Lys Ala Gly Gly Leu Lys Thr Ser Ser Ile Ile Ile
 130 135 140
 Ala Leu Thr Asp Gly Lys Leu Asp Gly Leu Val Pro Ser Tyr Ala Glu
 145 150 155 160
 Lys Glu Ala Lys Ile Ser Arg Ser Leu Gly Ala Ser Val Tyr Cys Val
 165 170 175
 Gly Val Leu Asp Phe Glu Gln Ala Gln Leu Glu Arg Ile Ala Asp Ser
 180 185 190
 Lys Glu Gln Val Phe Pro Val Lys Gly Gly Phe Gln Ala Leu Lys Gly
 195 200 205
 Ile Ile Asn Ser Ile Leu Ala Gln Ser Cys Thr Glu Ile Leu Glu Leu
 210 215 220
 Gln Pro Ser Ser Val Cys Val Gly Glu Glu Phe Gln Ile Val Leu Ser
 225 230 235 240
 Gly Arg Gly Phe Met Leu Gly Ser Arg Asn Gly Ser Val Leu Cys Thr
 245 250 255
 Tyr Thr Val Asn Glu Thr Tyr Thr Thr Ser Val Lys Pro Val Ser Val
 260 265 270
 Gln Leu Asn Ser Met Leu Cys Pro Ala Pro Ile Leu Asn Lys Ala Gly
 275 280 285
 Glu Thr Leu Asp Val Ser Val Ser Phe Asn Gly Gly Lys Ser Val Ile
 290 295 300
 Ser Gly Ser Leu Ile Val Thr Ala Thr Glu Cys Ser Asn Gly Ile Ala
 305 310 315 320
 Ala Ile Ile Val Ile Leu Val Leu Leu Leu Leu Gly Ile Gly Leu
 325 330 335
 Met Trp Trp Phe Trp Pro Leu Cys Cys Lys Val Val Ile Lys Asp Pro
 340 345 350

Pro Pro Pro Pro Pro Pro Ala Pro Lys Glu Glu Glu Glu Glu Pro Leu
 355 360 365
 Pro Thr Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly Gly Arg
 370 375 380
 Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Asp Lys Gly
 385 390 395 400
 Ser Thr Glu Glu Gly Ala Arg Leu Glu Lys Ala Lys Asn Ala Val Val
 405 410 415
 Lys Ile Pro Glu Glu Thr Glu Glu Pro Ile Arg Pro Arg Pro Pro Arg
 420 425 430
 Pro Lys Pro Thr His Gln Pro Pro Gln Thr Lys Trp Tyr Thr Pro Ile
 435 440 445
 Lys Gly Arg Leu Asp Ala Leu Trp Ala Leu Leu Arg Arg Gln Tyr Asp
 450 455 460
 Arg Val Ser Leu Met Arg Pro Gln Glu Gly Asp Glu Val Cys Ile Trp
 465 470 475 480
 Glu Cys Ile Glu Lys Glu Leu Thr Ala
 485

<210> 43
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FLAG tag

<400> 43

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 44
 <211> 137
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human mature J chain

<400> 44

Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys Ala
 1 5 10 15

Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp
 20 25 30

Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu
 35 40 45

Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr His

50 55 60
 Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp
 65 70 75 80
 Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser
 85 90 95
 Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala
 100 105 110
 Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala
 115 120 125
 Leu Thr Pro Asp Ala Cys Tyr Pro Asp
 130 135

 <210> 45
 <211> 137
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Mutant form of human mature J chain with C134S mutation compared
 to wild type Mature form of human J chain (SEQ ID NO:44)

 <400> 45
 Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys Ala
 1 5 10 15
 Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp
 20 25 30
 Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu
 35 40 45
 Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr His
 50 55 60
 Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp
 65 70 75 80
 Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser
 85 90 95
 Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala
 100 105 110
 Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala
 115 120 125
 Leu Thr Pro Asp Ala Ser Tyr Pro Asp
 130 135

 <210> 46
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>

<223> Mutant form of human mature J chain with amino acids 113-137
deleted compared to wild type Mature form of human J chain
(SEQ ID NO:44)

<400> 46

Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys Ala
1 5 10 15

Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp
20 25 30

Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu
35 40 45

Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr His
50 55 60

Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp
65 70 75 80

Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser
85 90 95

Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala
100 105 110

<210> 47

<211> 137

<212> PRT

<213> Artificial sequence

<220>

<223> Mutant form of human mature J chain with C109S and C134S
mutation compared to wild type mature form of human J chain
(SEQ ID NO:44)

<400> 47

Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys Ala
1 5 10 15

Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp
20 25 30

Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu
35 40 45

Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr His
50 55 60

Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp
65 70 75 80

Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser
85 90 95

Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Ser Tyr Thr Ala
100 105 110

Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala
 115 120 125

Leu Thr Pro Asp Ala Ser Tyr Pro Asp
 130 135

<210> 48
 <211> 248
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PWB2447 scFv

<400> 48
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Ser Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Val Ser Tyr Asp Gly Ser Asn Ile Tyr Tyr Ile Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Lys Ala Gly Arg Arg Thr Gln Leu Gln Pro Arg Asp Phe Leu Phe
 100 105 110
 Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 115 120 125
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr
 130 135 140
 Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr
 145 150 155 160
 Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln
 165 170 175
 Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg
 180 185 190
 Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr
 195 200 205
 Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr
 210 215 220

Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly
 225 230 235 240

Gly Thr Lys Leu Thr Val Leu Gly
 245

<210> 49
 <211> 251
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PWC2004 scFv

<400> 49
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Met Phe Thr Gly Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Lys Pro Tyr Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

His Asp Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Val Met Arg Leu Thr Ser Asp Asp Ser Ala Val Phe Tyr Cys
 85 90 95

Ala Arg Ser Arg Tyr Ser Ser Ser Pro Phe Arg Gly Gly Leu Asp Val
 100 105 110

Trp Gly Arg Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Ala Val Leu Thr
 130 135 140

Gln Pro Ser Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser
 145 150 155 160

Cys Thr Gly Ser Ser Ser Asn Ile Gly Asp Gly Tyr Asp Val His Trp
 165 170 175

Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn
 180 185 190

Thr Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser
 195 200 205

Asp Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Val Glu Asp Glu
 210 215 220

Ala Asp Tyr Phe Cys His Ser Tyr Asp Ser Ser Ile Ser Gly Trp Ile

Lys Leu Thr Val Leu Gly
245

<210> 51
<211> 244
<212> PRT
<213> Artificial sequence

<220>
<223> PWD0323 scFv

<400> 51

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gln Ile Trp Gly Arg Phe Glu Tyr Trp Gly Arg Gly Thr Thr
100 105 110
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125
Gly Gly Gly Ser Ala Gln Ala Val Leu Thr Gln Pro Ser Ser Ala Ser
130 135 140
Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser
145 150 155 160
Asn Ile Gly Thr Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr
165 170 175
Ala Pro Lys Leu Leu Ile Phe Ser Asn Asn Gln Arg Pro Ser Gly Val
180 185 190
Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Pro Ser Ala Ser Leu Ala
195 200 205
Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala
210 215 220
Trp Asp Asp Arg Leu Asn Gly Tyr Val Phe Gly Thr Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly

<210> 52
<211> 244
<212> PRT
<213> Artificial sequence

<220>
<223> PWD0422 scFv

<400> 52
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Thr Gln Ala Phe Ala Arg Phe Glu Phe Trp Gly Arg Gly Thr Leu
100 105 110
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125
Gly Gly Gly Ser Ala Gln Ser Val Val Thr Gln Pro Pro Ser Val Ser
130 135 140
Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser
145 150 155 160
Asn Ile Gly Thr Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr
165 170 175
Ala Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val
180 185 190
Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Val Ala
195 200 205
Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser
210 215 220
Trp Asp Asp Ser Leu Asn Gly Val Val Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly

<210> 53
<211> 244
<212> PRT
<213> Artificial sequence

<220>
<223> PWD0587 scFv

<400> 53
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gln Ile Trp Gly Arg Phe Glu Tyr Trp Gly Arg Gly Thr Thr
100 105 110
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125
Gly Gly Gly Ser Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser
130 135 140
Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser
145 150 155 160
Asn Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr
165 170 175
Ala Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val
180 185 190
Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala
195 200 205
Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala
210 215 220
Trp Asp Asp Ser Leu Asn Gly Val Val Phe Gly Gly Gly Thr Lys Leu
225 230 235 240
Thr Val Leu Gly

<210> 54
 <211> 248
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PWD0791 scFv

<400> 54

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Leu	Gln	Pro	Gly	Gly	1	5	10	15
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Ile	Ser	Tyr	20	25	30	
Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	35	40	45	
Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	50	55	60	
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	65	70	75	80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Arg	Val	Asp	His	Lys	Trp	Asp	Leu	Pro	Phe	Asp	Tyr	Trp	Gly	Arg	100	105	110	
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	115	120	125	
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ala	Leu	Ser	Tyr	Val	Leu	Thr	Gln	Pro	130	135	140	
Pro	Ser	Ala	Ser	Gly	Thr	Pro	Gly	Gln	Arg	Val	Val	Val	Ser	Cys	Ser	145	150	155	160
Gly	Gly	Ser	Ser	Asn	Ile	Gly	Lys	Asn	Pro	Val	Thr	Trp	Tyr	Gln	His	165	170	175	
Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Ser	Arg	Asn	Thr	Gln	Arg	180	185	190	
Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Thr	Ser	195	200	205	
Ala	Ser	Leu	Ala	Ile	Ser	Gly	Leu	Gln	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	210	215	220	
Tyr	Cys	Ala	Ala	Trp	Asp	Asp	Ser	Leu	Lys	Gly	Trp	Val	Phe	Gly	Gly	225	230	235	240
Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly												

<210> 55
 <211> 244
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PHD2222 scFv

<400> 55

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	1	5	10	15
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	20	25	30	
Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	35	40	45	
Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	50	55	60	
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	65	70	75	80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Arg	Gln	Ile	Trp	Gly	Arg	Phe	Glu	Tyr	Trp	Gly	Arg	Gly	Thr	Thr	100	105	110	
Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	115	120	125	
Gly	Gly	Gly	Ser	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Ala	Ser	130	135	140	
Gly	Thr	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	Ser	Gly	Ser	Ser	Ser	145	150	155	160
Asn	Ile	Gly	Ser	Asn	Thr	Val	Asn	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	165	170	175	
Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Asn	Asn	Gln	Arg	Pro	Ser	Gly	Val	180	185	190	
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	195	200	205	
Val	Ser	Gly	Leu	Gln	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Ala	210	215	220	
Trp	Asp	Asp	Ser	Leu	Asn	Gly	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	225	230	235	240
Thr	Val	Leu	Gly																

<210> 56
 <211> 244
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PHD2581 scFv

<400> 56

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	1	5	10	15
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	20	25	30	
Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	35	40	45	
Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	50	55	60	
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	65	70	75	80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Arg	Gln	Ile	Trp	Gly	Arg	Phe	Glu	Tyr	Trp	Gly	Lys	Gly	Thr	Met	100	105	110	
Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	115	120	125	
Gly	Gly	Gly	Ser	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Ala	Ser	130	135	140	
Gly	Thr	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	Ser	Gly	Ser	Ser	Ser	145	150	155	160
Asn	Ile	Gly	Ser	Asn	Thr	Val	Asn	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	165	170	175	
Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Asn	Asn	Gln	Arg	Pro	Ser	Gly	Val	180	185	190	
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	195	200	205	
Ile	Ser	Gly	Leu	Gln	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Ala	210	215	220	
Trp	Asp	Asp	Ser	Leu	Asn	Gly	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	225	230	235	240
Thr	Val	Leu	Gly																

<210> 57
 <211> 744
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DNA encoding PWB2447 scFv

<400> 57
 caggtgcagc tgggtggagtc tgggggaggc gtggtccagt ctgggggggtc cctgaggctc 60
 tcctgttcag cgtctggatt caccttcagt gactatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtc gtgtcatatg atggaagtaa tatatactat 180
 atagactccg tgaagggccg ttccaccatc tccagagacg attccaagaa cacgctttat 240
 ctccaaatga acagcctgag agctgaggac acggctctgt attactgtgc gaaagctggg 300
 aggcgaaccc aattacaacc cagagacttt ctttttgagt actggggcca aggaaccctg 360
 gtcaccgtct cgagtggtag aggcggttca ggcggagggt gcagcggcgg tggcggatcg 420
 tctgagctga ctcaggaccc tgctgtgtct gtggccttgg gacagacagt caggatcaca 480
 tgccaaggag acagcctcag aagctattat gcaagctggg accagcagaa gccaggacag 540
 gccctgtac ttgtcatcta cggtaaaaac aaccggccct cagggatccc agaccgattc 600
 tctggctcca gctcaggaaa cacagcttcc ttgaccatca ctggggctca ggcggaagat 660
 gaggtgact attactgtaa ctcccgggac agcagtggta accatgtggg attcggcgga 720
 gggaccaagc tgaccgtcct aggt 744

<210> 58
 <211> 753
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DNA encoding PWC2004 scFv

<400> 58
 caggtccagc tgggtgcagtc tggggctgag gtgaggaagc ctggggcctc agtgaaggctc 60
 tcctgcaagg cttctggata catgttcacc ggctactata tgcactgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggatgg atcaagcctt acagtggtag cacaactat 180
 gcacagaagt ttcacgacag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
 atggagggtga tgaggctgac atctgacgac agcgcctgtg tttactgtgc gagaagccgc 300
 tatagcagca gcccttttag ggggggtttg gacgtctggg gccgagggac aatggtcacc 360
 gtctcgagtg gaggcggcgg ttcaggcgga ggtggetctg gcggtggcgg aagtgcacag 420

gctgtgctga ctcagccgtc ctcagtgtct ggggccccag ggcagagggg caccatctcc 480
 tgcactggga gcagctccaa catcggggac gggtatgatg tccactggta tcagcaactt 540
 ccaggaacag ccccccact cctcatctat ggtaacacta atcggccctc aggggtccct 600
 gaccgattct ctggctccaa gtctgacacc tctgcctccc tggccatcac tgggtccag 660
 gttgaggatg aggctgatta tttctgccac tcctatgaca gcagtatcag tggctggatt 720
 ttggcgaggag ggaccaaggc caccgtccta ggt 753

<210> 59
 <211> 738
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DNA encoding PWD0283 scFv

<400> 59
 gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
 tcctgtgcag cctctggatt caccctttagc agctatgcca cgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagtgggg 300
 ggagccattc gctttgactc ctggggcagg ggaaccctgg tcaccgtctc gagtggaggc 360
 ggcggttcag gcggagggtg ctctggcggt ggcggaagtg cactttccta tgagctgact 420
 cagccaccct cagcgtctga gacccccggg cagaggggtc ccatctcttg ttctggaggc 480
 acctcgaaca tcggatccaa cactatcaac tgggtaccagc aggtcccagg aacggccccc 540
 aaactactca tctattttaa taatcggcgg cccgcagggg tccctgcccg attttctgcc 600
 tccaagtctg gcacctcagc ctccctgacc atcagtgggc tccagtctga ggatgaggct 660
 gactattatt gttcagcatg ggatgacagc ctgagtggcg tgggtgttcgg cggagggacc 720
 aagctgaccg tcctaggt 738

<210> 60
 <211> 732
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DNA encoding PWD0323 scFv

<400> 60

gaggtgcagc tgttggagtc tgggggagggc ttggtacagc ctgggggggtc cctgagactc	60
tctgtgcag cctctggatt caccttttagc agctatgccca tgagctgggt cccccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gaggcaaadc	300
tggggacgat ttgaatattg ggggaggggg accacgggtca ccgtctcgag tggaggcggc	360
gggttcaggcg gaggtggctc tggcggtggc ggaagtgcac aggtctgtgt gactcagccg	420
tctcagcgt ctgggacccc cgggcagagg gtcaccatct cttgttctgg aagcagctcc	480
aacatcgga ctaatactgt aaactggtac caacagctcc caggaacggc ccccaaactc	540
ctcatcttta gtaataatca acggccctca ggggtccctg accgattctc tggctccaag	600
tctggccct cagcctccct ggccatcagt ggactccagt ccgaggatga ggctgattat	660
tactgtgcag catgggatga caggctgaat ggttatgtct tcggaactgg gaccaagctg	720
accgtcctag gt	732

<210> 61
 <211> 732
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DNA encoding PWD0422 scFv

<400> 61	
gaggtgcagc tgttggagtc tgggggagggc ttggtacagc ctgggggggtc cctgagactc	60
tctgtgcag cctctggatt caccttttagc agctatgccca tgagctgggt cccccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gaccagggc	300
tttctcgtt tcaggttttg gggccggggc accctgggtca ccgtctcgag tggaggcggc	360
gggttcaggcg gaggtggctc tggcggtggc ggaagtgcac agtctgtcgt gacgcagccg	420
ccctcagtgt ctgggacccc cgggcagagg gtcaccatct cttgttctgg aagcagctcc	480
aacatcgga ctaatactgt aaactggtac caacaactcc caggaacggc ccccaaactc	540
ctcatctata gtaataatca gcgaccctca ggggtccctg accgattctc tggctccaag	600
tctggcacct cagcctccgt ggccatcagt gggctccagt ctgaggatga ggctgattac	660
tactgttctt catgggatga cagcctgaat ggcgtcgtgt tcggcgagg gaccaagctg	720

accgtcctag gt

732

<210> 62
<211> 732
<212> DNA
<213> Artificial sequence

<220>
<223> DNA encoding PWD0587 scFv

<400> 62
gaggtgcagc tggttgagtc tgggggagggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttttagc agctatgcc a tgagctgggt ccgccaggct 120
ccaggaaggg ggctggagtg ggtctcagct attagtggta gtgggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gaggcaaata 300
tggggacgat ttgaatattg gggggcggggg accacgggtca ccgtctcgag tggaggcggc 360
gggtcaggcg gaggtggctc tggcgggtggc ggaagtgcac agtctgtgct gactcagcca 420
ccctcagcgt ctgggacccc cgggcagagg gtcaccatct cttgttctgg aagcagctcc 480
aacatcggaa gtaatactgt aaactggtag cagcagctcc caggaacggc ccccaaactc 540
ctcatctata gtaataatca gcggccctca ggggtccctg accgattctc tggctccaag 600
tctggcacct cagcctccct ggccatcagt gggctccagt ctgaggatga ggctgattat 660
tactgtgcag catgggatga cagcctgaat ggagtggat tcggcggagg gaccaagctg 720
accgtcctag gt 732

<210> 63
<211> 744
<212> DNA
<213> Artificial sequence

<220>
<223> DNA encoding PWD0791 scFv

<400> 63
gaggtgcagc tggttgagtc tgggggagggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt ctctttttatc agctatgcc a tgagctgggt ccgccaggct 120
ccaggaaggg ggctggagtg ggtctcagct attagtggta gtgggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc cagagtggac 300

cataaatggg acctaccctt tgactactgg ggccgaggca ccttgggtcac cgtctcgagt	360
ggaggcgggc gttcaggcgg aggtggctct ggcggtggcg gaagtgcact ttcctatgtg	420
ctgactcagc caccctcagc gtctggaacc cccgggcaga gggtcgtcgt ctcttgttct	480
gggggcagct ccaacatcgg aaaaaatcct gtaacctggt atcagcacct cccaggaacg	540
gccccaaac tcctcatctc tagaaatact cagcggccct caggagtccc tgaccgattc	600
tctggctcca agtctggcac gtcagcctcc ctggccatca gtgggctcca gtctgaggat	660
gaggctgatt attactgtgc agcatgggat gacagcctca agggctgggt gttcggcgga	720
gggaccaagc tgaccgtcct aggt	744

<210> 64
 <211> 732
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DNA encoding PHD2222 scFv

<400> 64	
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc	60
tcctgtgcag cctctggatt caccttttagc agctatgcc a tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtagtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gaggcaaatc	300
tggggacgct ttgaatattg ggggcggggg accacgggtca ccgtctcgag tggaggcggc	360
ggttcaggcg gaggtggctc tggcggtggc ggaagtgcac agtctgtgct gactcagcca	420
ccctcagcgt ctgggacccc cgggcagagg gtcaccatct cttgttcttg aagcagctcc	480
aacatcggaa gtaatactgt aaactggtac cagcagctcc caggaacggc ccccaaactc	540
ctcatctata gtaataatca gcggccctca ggggtccctg accgattctc tggtccaag	600
tctggcacct cagcctccct ggccgtcagt gggctccagt ctgaggatga ggctgattat	660
tactgtgcag catgggatga cagcctgaat ggtgtggtat tcggcggagg gaccaagctg	720
accgtcctag gt	732

<210> 65
 <211> 732
 <212> DNA
 <213> Artificial sequence

<220>

<223> DNA encoding PHD2581 sequence

<400> 65

gaggtgcagc	tgttggagtc	tgggggaggc	ttggtacagc	ctgggggggc	cctgagactc	60
tcctgtgcag	cctctggatt	cacctttagc	agctatgcc	tgagctgggt	ccgccaggct	120
ccaggaagg	ggctggagtg	ggtctcagct	attagtggta	gtggtggtag	cacatactac	180
gcagactccg	tgaagggccg	gttcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggccgtgt	attactgtgc	gaggcaaata	300
tggggacgat	ttgaatattg	gggcaaagg	acaatggta	ccgtctcgag	tggaggcggc	360
ggttcaggcg	gaggtggctc	tggcgggtgc	ggaagtgcac	agtctgtgct	gactcagcca	420
ccctcagcgt	ctgggacccc	cgggcagagg	gtcaccatct	cttggtcttg	aagcagctcc	480
aacatcgga	gtaatactgt	aaactggtac	cagcagctcc	caggaacggc	ccccaaactc	540
ctcatctata	gtaataatca	gcggccctca	ggggcccttg	accgattctc	tggctccaag	600
tctggcacct	cagcctccct	ggccatcagt	gggctccagt	ctgaggatga	ggctgattat	660
tactgtgcgg	catgggatga	cagcctgaat	ggtgtgggat	tcggcggagg	gaccaagctg	720
accgtcctag	gt					732